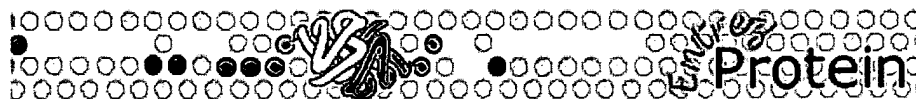


(FILE 'HOME' ENTERED AT 13:36:45 ON 20 OCT 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 13:36:48 ON 20 OCT 2004

L1	301 S PYRF
L2	127 S L1 (10N) (DEFECT? OR MUTA?)
L3	53 S L2 AND (AUXO?)
L4	12 S L3 AND (CORIOLUS OR POLYPORUS OR TRAMETES OR FUNG?)
L5	6 DUP REM L4 (6 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:39:39 ON 20 OCT 2004



Entrez

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Protein

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Clusters of orthologous
groupsProtein reviews on the
webSearch for full length
cDNAs☐ 1: [XP_401829](#)[BLink](#), [Domains](#), [Links](#)

PYRF_USTMA Orotidine 5"-phosphate decarboxylase (OMP
decarboxylase) (OMPDCase) (OMPdecase) (Uridine 5"-monophosphate
synthase) (UMP synthase) [Ustilago maydis 521]
[gi|49075542|ref|XP_401829.1|](#)[\[49075542\]](#)

☐ 2: [EAK85218](#)[BLink](#), [Domains](#), [Links](#)

PYRF_USTMA Orotidine 5"-phosphate decarboxylase (OMP
decarboxylase) (OMPDCase) (OMPdecase) (Uridine 5"-monophosphate
synthase) (UMP synthase) [Ustilago maydis 521]
[gi|46099985|gb|EAK85218.1|](#)[\[46099985\]](#)

☐ 3: [CAC32408](#)[BLink](#), [Links](#)

unnamed protein product [Trametes versicolor]
[gi|13157814|emb|CAC32408.1|](#)[\[13157814\]](#)

Basidiomycetes + PYRF
(protein)

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Oct 13 2004 06:44:09



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cDNAs☐ 1: [XM_401829](#)

Links

Ustilago maydis 521, UM04214.1 predicted mRNA
gi|49075541|ref|XM_401829.1|[49075541]☐ 2: [AACP01000149](#)

Links

Ustilago maydis 521 chromosome 12 cont1.149_scaffold11, whole genome
shotgun sequence
gi|33302107|gb|AACP01000149.1|[33302107]☐ 3: [AX078058](#)

Links

Sequence 2 from Patent WO0107620
gi|13157813|emb|AX078058.1||pat|WO|0107620|2|[13157813]☐ 4: [AX078057](#)

Links

Sequence 1 from Patent WO0107620
gi|13157812|emb|AX078057.1||pat|WO|0107620|1|[13157812]

Basidiomycetes + pyrF

c-multiple

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Oct 13 2004 06:44:09



ENZYME: 2.4.2.10

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Entry EC 2.4.2.10
Name orotate phosphoribosyltransferase
 orotidylic acid phosphorylase
 orotidine-5'-phosphate pyrophosphorylase
 OPRase
 orotate phosphoribosyl pyrophosphate transferase
 orotic acid phosphoribosyltransferase
 orotidine 5'-monophosphate pyrophosphorylase
 orotidine monophosphate pyrophosphorylase
 orotidine phosphoribosyltransferase
 orotidylate phosphoribosyltransferase
 orotidylate pyrophosphorylase
 orotidylic acid pyrophosphorylase
 orotidylic phosphorylase
 orotidylic pyrophosphorylase
Class Transferases
 Glycosyltransferases
 Pentosyltransferases
Sysname orotidine-5'-phosphate:diphosphate
 \$phospho-alpha-D-ribosyl-transferase
Reaction orotidine 5'-phosphate + diphosphate = orotate +
 5-phospho-alpha-D-ribose 1-diphosphate
 [RN:R01870]
Substrate orotidine 5'-phosphate [CPD:C01103]
 diphosphate [CPD:C00013]
Product orotate [CPD:C00295]
 5-phospho-alpha-D-ribose 1-diphosphate [CPD:C00119]
Comment The enzyme from higher eukaryotes also catalyses the reaction
 listed as EC 4.1.1.23, orotidine-5'-phosphate decarboxylase.
Pathway PATH: map00240 Pyrimidine metabolism
Ortholog KO: K00762 orotate phosphoribosyltransferase
Genes HSA: 7372 (UMPS)
 MMU: 22247 (Umps)
 CEL: R12E2.11 T07C4.1
 CME: CMK046C
 SCE: YML106W (URA5) YMR271C (URA10)
 AGO: AER290C (AER290Cp)
 CAL: orf19.2555 (URA5)
 SPO: SPBC725.15
 PFA: PFE0630c
 ECO: b3642 (pyrE)
 ECJ: JW3617 (pyrE)
 ECE: Z5066 (pyrE)
 ECS: ECS4517
 ECC: c4466 (pyrE)
 STY: STY4061 (pyrE)
 STT: t3785 (pyrE)
 STM: STM3733 (pyrE)
 YPE: YPO0045 (pyrE)
 YPK: y0096 (pyrE)
 YPM: YP0046 (pyrE)
 YPS: YPTB0042 (pyrE)
 SFL: SF3681 (pyrE)
 SFX: S4087 (pyrE)
 ECA: ECA0141 (pyrE)
 PLU: plu4869 (pyrE)
 BUC: BU559 (pyrE)
 BAB: bbp506 (pyrE)
 WBR: Wbr0361 (pyrE)
 HIN: HI0272 (pyrE)
 HDU: HD1759 (pyrE)
 PMU: PM1877 (pyrE)

XFA: XF0153
XFT: PD0122 (pyrE)
XCC: XCC3847 (pyrE)
XAC: XAC3903 (pyrE)
VCH: VC0211
VVU: VV10831
VVY: VV0280
VPA: VP0178
PPR: PBPRA0199
PAE: PA5331 (pyrE)
PPU: PP5291 (pyrE)
PST: PSPT00080 (pyrE)
ACI: ACIAD3525 (pyrE)
SON: SO4255 (pyrE)
CBU: CBU0296 (pyrE)
LPN: lpg1204 (pyrE)
MCA: MCA2740 (pyrE)
NME: NMB1874
NMA: NMA0582 (pyrE)
CVI: CV4248 (pyrE)
RSO: RS01009 (pyrE)
BMA: BMA2587 (pyrE)
BPS: BPSL3243 (pyrE)
BPE: BP0370 (pyrE)
BPA: BPP4060 (pyrE)
BBR: BB4533 (pyrE)
NEU: NE1734 (pyrE)
HPY: HP1257 (pyrE)
HPJ: jhp1178
HHE: HH1355 (pyrE)
WSU: WS0315 (pyrE)
CJE: Cj0233c (pyrE)
GSU: GSU1637 (pyrE)
DVU: DVU2943 (pyrE)
BBA: Bd0896 Bd0979 (pyrE)
DPS: DP2916
WOL: WD0228 (pyrE)
MLO: mll5916 mlr7756
SME: SMC02165 (pyrE)
ATU: Atu0400 (pyrE)
ATC: AGR_C_704
BME: BMEI1295
BMS: BR0653 (pyrE)
BJA: blr8134 (pyrE)
RPA: RPA4724 (pyrE)
BHE: BH05050 (pyrE)
BQU: BQ04240 (pyrE)
CCR: CC1555
BSU: BG10720 (pyrE)
BHA: BH2532 (pyrE)
BAN: BA4021 (pyrE)
BAR: GBAA4021 (pyrE)
BAA: BA_4492
BAT: BAS3733
BCE: BC3882
BCA: BCE0690 BCE3927 (pyrE)
BCZ: BTZK0532 (pyrE) BTZK3641 (pyrE)
BTK: BT9727_0532 (pyrE) BT9727_3624 (pyrE)
OIH: OB1495 (pyrE)
SAU: SA1048 (pyrE)
SAV: SAV1205 (pyrE)
SAM: MW1088 (pyrE)
SAR: SAR1181 (pyrE)
SAS: SAS1139
SEP: SE0881
LMO: lmo1831 (pyrE)
LMF: LMOF2365_1859 (pyrE)
LIN: lin1945 (pyrE)
LLA: L80411 (pyrE)
SPY: SPY0901 (pyrE)
SPM: spyM18_0960 (pyrE)

SPG: SpyM3_0617 (pyrE)
SPS: SPs1236
SPA: M6_Spy0721
SPN: SP0702
SPR: spr0614 (pyrE)
SAG: SAG1046 (pyrE)
SAN: gbs1081 (pyrE)
SMU: SMU.1221 (pyrE)
LPL: lp_2697 (pyrE)
LJO: LJ1283
EFA: EF1712 (pyrE)
CAC: CAC0027 (pyrE)
CPE: CPE1177 (pyrE)
CTC: CTC02378
TTE: TTE1529 (pyrE)
MPE: MYPE7840 (pyrE)
MTU: Rv0382c (umpA)
MTC: MT0395
MBO: Mb0389c (pyrE)
MLE: ML2487
MPA: MAP3857 (umpA)
CGL: NCgl2676 (Cgl2773)
CEF: CE2604
CDI: DIP2097 (pyrE)
SCO: SCO3650 (SCH10.28c)
SMA: SAV4522 (pyrE)
TWH: TW743 (umpA)
TWS: TW755 (pyrE)
LXX: Lxx23400 (pyrE)
PAC: PPA1004
BLO: BL0788 (pyrE)
FNU: FN0427
RBA: RB328 (pyrE)
CPN: CPn0608
CPA: CP0139
CPJ: CPj0608
CPT: CpB0632
CCA: CCA00132 (pyrE)
TDE: TDE1001 (pyrE)
LIL: LA1539 LA2988 (pyrE)
LIC: LIC11076 (pyrE) LIC12227
BTH: BT3731
PGI: PG1353 (pyrE)
SYN: slr0185 (umpS)
SYW: SYNW0238 (pyrE)
SYC: syc1518_d (umpS)
TEL: tlr1828
GVI: gll14276 glr1079
ANA: alr2945 alr5099
PMA: Pro0307 (pyrE)
PMM: PMM0275 (pyrE)
PMT: PMT1868 (pyrE)
CTE: CT0083 (pyrE)
DRA: DR0447
TTH: TTC1380
AAE: aq_1907
TMA: TM0331
MJA: MJ1109 (pyrE) MJ1646
MMP: MMP0079 MMP1492 (pyrE)
MAC: MA0919 MA2520 (pyrE) MA3307 (pyrE)

MMA: MM0142-MM2035
MTH: MTH1860 MTH876
MKA: MK1072 (pyrE)
AFU: AF0386 AF1741 (pyrE)
HAL: VNG0448G (pyrE1) VNG2118G (pyrE2)
TAC: Ta0056 Tal164
TVO: TVG0009630 TVG1281244
PTO: PTO0208 PTO0465
PHO: PH1128
PAB: PAB2430 (pyrE)
PFU: PF1034

APE: APE2349
SSO: SSO0615 (pyrE)
STO: ST1481
PAI: PAE3264 (pyrE)

Disease MIM: 258900 Uridine monophosphate synthetase (orotate
phosphoribosyl transferase

Motif PS: PS00103 [LIVMFYWCTA] - [LIVM] - [LIVMA] - [LIVMFC] - [DE] - D - [LIVMS] -
[LIVM] - [STAVD] - [STAR] - [GAC] - x - [STAR]

PS: PS00156 [LIVMFTAR] - [LIVMF] - x - D - x - K - x (2) - D - [IV] - [ADGP] - x - T -
[CLIVMNTA]

Structures PDB: 1LH0 1OPR 1ORO 1STO

Reference 1 [PMID:692383]

Jones, M.E., Kavipurapu, P.R. and Traut, T.W. Orotate
phosphoribosyltransferase: orotidylate decarboxylase (Ehrlich
ascites cell). Methods Enzymol. 51 (1978) 155-167.

2

Lieberman, I., Kornberg, A. and Simms, E.S. Enzymatic synthesis of
pyrimidine nucleotides. Orotidine-5'-phosphate and
uridine-5'-phosphate. J. Biol. Chem. 215 (1955) 403-415.

3 [PMID:6893554]

McClard, R.W., Black, M.J., Livingstone, L.R. and Jones, M.E.
Isolation and initial characterization of the single polypeptide
that synthesizes uridine 5'-monophosphate from orotate in Ehrlich
ascites carcinoma. Purification by tandem affinity chromatography
of uridine-5'-monophosphate synthase. Biochemistry 19 (1980)
4699-4706.

Other DBs IUBMB Enzyme Nomenclature: 2.4.2.10

ExPASy - ENZYME nomenclature database: 2.4.2.10

ERGO genome analysis and discovery system: 2.4.2.10

BRENDA, the Enzyme Database: 2.4.2.10

CAS: 9030-25-5

LinkDB

All DBs

=> Text only

[KEGG | DBGET | GenomeNet]

Seq 19 10:3

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	485	41.9	225	2	A36459	orotate phosphorib
2	462.5	39.9	226	1	XJBY5	orotate phosphorib
3	458	39.6	213	2	A82981	orotate phosphorib
4	454	39.2	213	2	S32801	orotate phosphorib
5	453	39.1	213	1	XJEC	orotate phosphorib
6	452	39.0	213	2	E91193	orotate phosphorib
7	452	39.0	213	2	F86040	orotate phosphorib
8	452	39.0	214	2	E82350	orotate phosphorib
9	451	38.9	215	2	AF0006	orotate phosphorib
10	449	38.8	233	1	S30118	orotate phosphorib
11	446	38.5	213	2	AH0970	orotate phosphorib
12	446	38.5	215	2	T40667	orotate phosphorib
13	432	37.3	213	2	I64058	orotate phosphorib
14	428.5	37.0	227	1	XJBY10	orotate phosphorib
15	428.5	37.0	232	1	JS0175	orotate phosphorib
16	426	36.8	219	2	S55840	orotate phosphorib
17	422.5	36.5	213	2	H81032	probable orotate p
18	416.5	36.0	231	1	A29459	orotate phosphorib
19	414.5	35.8	236	1	S13091	orotate phosphorib
20	398	34.4	219	2	H82840	orotate phosphorib
21	381.5	32.9	213	2	A84995	orotate phosphorib
22	366	31.6	224	2	C96903	orotate phosphorib
23	218	18.8	458	2	T30520	probable orotate p
24	209	18.0	461	2	T02058	UMP synthase - com
25	207.5	17.9	476	2	S46440	bifunctional UMP s
26	204.5	17.7	476	2	T47606	UMP synthase - Ara
27	203.5	17.6	186	2	B71054	probable orotate p
28	203	17.5	182	2	B75089	probable orotate p
29	197	17.0	182	2	T47129	orotate phosphorib
30	194.5	16.8	195	2	G90208	orotate phosphorib
31	194	16.8	480	1	A30148	UMP synthase - hum
32	188	16.2	480	1	JN0558	UMP synthase - bov
33	181.5	15.7	478	1	S03826	UMP synthase - sli
34	181	15.6	175	2	F84361	orotate phosphorib
35	181	15.6	178	2	D69467	probable orotate p
36	174.5	15.1	178	2	B72463	probable orotate p
37	171.5	14.8	180	2	H69115	probable orotate p
38	170	14.7	209	2	AG1675	orotate phosphorib
39	169.5	14.6	210	2	F97948	orotate phosphorib
40	169.5	14.6	227	2	T33094	probable orotate p
41	166.5	14.4	212	1	A60993	orotate phosphorib
42	165.5	14.3	209	2	D86758	orotate phosphorib

not
PYR F

43	165.5	14.3	210	2	D95081
44	160	13.8	209	2	AG1303
45	159	13.7	493	1	JU0141

orotate phosphorib
orotate phosphorib
UMP synthase - fru

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	485	41.9	225	1	PYRE_CRYNE	P18132 cryptococcu
2	464	40.1	215	1	PYRE_SHEON	Q8e9l5 shewanella
3	462.5	39.9	226	1	PYRE_YEAST	P13298 saccharomyc
4	462	39.9	213	1	PYRE_VIBPA	Q87t92 vibrio para
5	460.5	39.8	226	1	PYRE_KLULA	O13474 kluyveromyc
6	458	39.6	213	1	PYRE_PSEAE	P50587 pseudomonas
7	458	39.6	213	1	PYRE_VIBVU	Q8ddx5 vibrio vuln
8	452	39.0	212	1	PYRE_SALTY	P08870 salmonella
9	452	39.0	214	1	PYRE_VIBCH	Q9kvd5 vibrio chol
10	451	38.9	212	1	PYRE_ECOLI	P00495 escherichia
11	451	38.9	215	1	PYRE_YERPE	Q8zjp7 yersinia pe
12	450	38.9	212	1	PYRE_ECO57	Q8xd99 escherichia
13	449	38.8	233	1	PYRE_COLGR	P35788 colletotric
14	449	38.8	238	1	PYRE_COCPO	O93849 coccidioide
15	446	38.5	215	1	PYRE_SCHPO	O94331 schizosacch
16	445	38.4	213	1	PYRE_PSEPK	Q88c92 pseudomonas
17	444	38.3	212	1	PYRE_SALTI	Q8z2h5 salmonella
18	442.5	38.2	183	1	PYRE_METCA	Q8vr31 methylococc
19	435.5	37.6	234	1	PYRE_METAN	O42767 metarhizium
20	432	37.3	213	1	PYRE_HAEIN	P43855 haemophilus
21	429	37.0	213	1	PYRE_PSESM	Q88bd7 pseudomonas
22	428.5	37.0	227	1	PYRX_YEAST	P30402 saccharomyc
23	428.5	37.0	232	1	PYRE_SORMA	P18904 sordaria ma
24	426	36.8	219	1	PYRE_YARLI	P41923 yarrowia li
25	422.5	36.5	213	1	PYRE_NEIMA	Q9j25 neisseria m
26	414.5	35.8	236	1	PYRE_TRIRE	P21846 trichoderma
27	413	35.7	214	1	PYRE_PASMU	Q9c2w4 pasteurella
28	403.5	34.8	231	1	PYRE_PODAN	P08309 podospira a
29	399.5	34.5	219	1	PYRE_XANCP	Q8p469 xanthomonas
30	398	34.4	219	1	PYRE_XYLFA	Q9pgz3 xylella fas
31	398	34.4	231	1	PYRE_BIFLO	Q8g661 bifidobacte
32	397	34.3	219	1	PYRE_XANAC	Q8pfs5 xanthomonas
33	392	33.9	226	1	PYRE_RALSO	Q8y342 ralstonia s
34	391	33.8	219	1	PYRE_XYLFT	Q87f16 xylella fas
35	381.5	32.9	213	1	PYRE_BUCAI	P57622 buchnera ap
36	366	31.6	224	1	PYRE_CLOAB	Q97n11 clostridium
37	272	23.5	206	1	PYRE_BUCBP	P59575 buchnera ap
38	262.5	22.7	193	1	PYRE_PYRAE	Q8ztg3 pyrobaculum
39	239.5	20.7	183	1	PYRE_METKA	P58860-methanopyru
40	218	18.8	197	1	PYRE_SULAC	O08359 sulfolobus
41	212.5	18.4	195	1	PYRE_SULTO	Q970x1 sulfolobus
42	209	18.0	461	1	PYR5_TOBAC	Q42942 nicotiana t
43	204.5	17.7	476	1	PYR5_ARATH	Q42586 arabidopsis
44	203.5	17.6	186	1	PYRE_PYRHO	O58855 pyrococcus
45	203	17.5	182	1	PYRE_PYRAB	P56814 pyrococcus

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	516.5	44.6	244	3	074686	074686	ajellomyces
2	490	42.3	225	3	Q870L6	Q870L6	cryptococcu
3	486	42.0	225	3	Q870L7	Q870L7	cryptococcu
4	485	41.9	225	3	Q870L8	Q870L8	cryptococcu
5	484	41.8	225	3	O13404	O13404	cryptococcu
6	482	41.6	225	3	Q92230	Q92230	cryptococcu
7	479	41.4	225	3	O13405	O13405	cryptococcu
8	478	41.3	225	3	O13406	O13406	cryptococcu
9	477	41.2	225	3	Q92232	Q92232	cryptococcu
10	477	41.2	225	3	Q86ZQ7	Q86ZQ7	cryptococcu
11	474	40.9	225	3	Q870L9	Q870L9	cryptococcu
12	473.5	40.9	224	3	Q00524	Q00524	cryptococcu
13	473	40.8	225	3	Q92231	Q92231	cryptococcu
14	472	40.8	218	3	O13487	O13487	mucor circi
15	465	40.2	208	3	Q9UW68	Q9UW68	cryptococcu
16	465	40.2	210	3	Q9UW60	Q9UW60	cryptococcu
17	465	40.2	211	3	Q9UQW8	Q9UQW8	cryptococcu
18	464	40.1	210	3	Q9UQZ3	Q9UQZ3	cryptococcu
19	461	39.8	200	3	Q9UW69	Q9UW69	cryptococcu
20	458.5	39.6	206	3	Q9UW50	Q9UW50	cryptococcu
21	455.5	39.3	198	3	Q9UW47	Q9UW47	cryptococcu
22	455.5	39.3	200	3	Q9UW59	Q9UW59	cryptococcu
23	455.5	39.3	206	3	Q9UW52	Q9UW52	cryptococcu
24	455.5	39.3	207	3	Q9UW61	Q9UW61	cryptococcu
25	455.5	39.3	208	3	Q9UW57	Q9UW57	cryptococcu
26	455.5	39.3	209	3	Q9UR57	Q9UR57	cryptococcu
27	455.5	39.3	209	3	Q9UW58	Q9UW58	cryptococcu
28	455.5	39.3	211	3	Q9UQX9	Q9UQX9	cryptococcu
29	455.5	39.3	212	3	Q9UW67	Q9UW67	cryptococcu

30	455.5	39.3	212	3	Q9UW54	Q9uw54 cryptococcu
31	454	39.2	213	16	Q7UAZ8	Q7uaz8 shigella fl
32	454	39.2	218	16	Q83J15	Q83jl5 shigella fl
33	453.5	39.2	204	3	Q9UW51	Q9uw51 cryptococcu
34	452.5	39.1	199	3	Q9UW49	Q9uw49 cryptococcu
35	450.5	38.9	192	3	Q9UW66	Q9uw66 cryptococcu
36	450.5	38.9	203	3	Q9UW46	Q9uw46 cryptococcu
37	449.5	38.8	245	3	O93848	O93848 exophiala d
38	445	38.4	213	16	Q88C92	Q88c92 pseudomonas
39	429	37.0	213	16	Q88BD7	Q88bd7 pseudomonas
40	409	35.3	224	16	Q7VSN4	Q7vsn4 bordetella
41	408	35.2	213	16	Q7VKV3	Q7vkv3 haemophilus
42	399	34.5	235	16	Q7W3H5	Q7w3h5 bordetella
43	398	34.4	235	16	Q7WEU9	Q7weu9 bordetella
44	397.5	34.3	158	3	Q9UW62	Q9uw62 cryptococcu
45	380.5	32.9	157	3	Q9UW53	Q9uw53 cryptococcu

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1158	100.0	227	4	AAB46894	Aab46894 T. versic
2	504.5	43.6	216	6	ABU16739	Abu16739 Protein e
3	504.5	43.6	247	6	ADA33758	Ada33758 Acinetoba
4	458	39.6	213	6	ABU38902	Abu38902 Protein e
5	453	39.1	213	4	AAB75103	Aab75103 E. coli o
6	453	39.1	213	6	ABU28822	Abu28822 Protein e
7	452	39.0	214	6	ABU49061	Abu49061 Protein e
8	451	38.9	213	6	ABU31219	Abu31219 Protein e
9	451	38.9	215	6	ABU50113	Abu50113 Protein e
10	446	38.5	213	6	ABU45257	Abu45257 Protein e
11	446	38.5	213	6	ABU48380	Abu48380 Protein e
12	439	37.9	213	6	ABU28226	Abu28226 Protein e
13	437	37.7	214	6	ABM68819	Abm68819 Photorhab
14	434	37.5	214	6	ABU41157	Abu41157 Protein e
15	432.5	37.3	218	5	ABP74016	Abp74016 Candida a

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	504.5	43.6	247	4	US-09-328-352-5045	Sequence 5045, Ap	
2	458	39.6	222	4	US-09-252-991A-23841	Sequence 23841, A	
3	458	39.6	277	4	US-09-489-039A-10600	Sequence 10600, A	
4	414	35.8	201	4	US-09-543-681A-7516	Sequence 7516, Ap	
5	230.5	19.9	443	4	US-09-675-018B-12	Sequence 12, Appl	
6	207.5	17.9	476	4	US-09-675-018B-13	Sequence 13, Appl	
7	207.5	17.9	476	4	US-09-675-018B-14	Sequence 14, Appl	
8	203	17.5	478	4	US-09-675-018B-6	Sequence 6, Appli	
9	197.5	17.1	476	4	US-09-675-018B-8	Sequence 8, Appli	
10	197.5	17.1	476	4	US-09-675-018B-10	Sequence 10, Appl	
11	162.5	14.0	211	4	US-09-107-532A-5221	Sequence 5221, Ap	
12	160.5	13.9	257	4	US-09-134-000C-6094	Sequence 6094, Ap	
13	154	13.3	183	2	US-08-912-794-2	Sequence 2, Appli	
14	137.5	11.9	182	1	US-08-790-309-2	Sequence 2, Appli	
15	137.5	11.9	182	4	US-09-250-585A-2	Sequence 2, Appli	

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	504.5	43.6	216	12	US-10-282-122A-44663	Sequence 44663, A	
2	458	39.6	213	12	US-10-282-122A-66826	Sequence 66826, A	
3	453	39.1	213	12	US-10-282-122A-56746	Sequence 56746, A	
4	452	39.0	214	12	US-10-282-122A-76985	Sequence 76985, A	
5	451	38.9	213	12	US-10-282-122A-59143	Sequence 59143, A	
6	451	38.9	215	12	US-10-282-122A-78037	Sequence 78037, A	
7	446	38.5	213	12	US-10-282-122A-73181	Sequence 73181, A	
8	446	38.5	213	12	US-10-282-122A-76304	Sequence 76304, A	
9	439	37.9	213	12	US-10-282-122A-56150	Sequence 56150, A	
10	434	37.5	214	12	US-10-282-122A-69081	Sequence 69081, A	
11	432.5	37.3	218	14	US-10-032-585-7853	Sequence 7853, Ap	
12	419.5	36.2	194	12	US-10-282-122A-63159	Sequence 63159, A	
13	413	35.7	214	12	US-10-282-122A-67430	Sequence 67430, A	
14	405.5	35.0	210	12	US-10-282-122A-61357	Sequence 61357, A	
15	366	31.6	224	12	US-10-282-122A-51589	Sequence 51589, A	

SEQ ID NO: 3

RESULT 1

A36459

orotate phosphoribosyltransferase (EC 2.4.2.10) URA5 [validated] - fungus
(*Filobasidium floriforme*)

C;Species: Filobasidiella neoformans, Cryptococcus neoformans

C;Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 31-Mar-2000

C;Accession: A36459

R;Edman, J.C.; Kwon-Chung, K.J.

Mol. Cell. Biol. 10, 4538-4544, 1990

A;Title: Isolation of the URA5 gene from *Cryptococcus neoformans* var. *neoformans* and its use as a selective marker for transformation.

A;Reference number: A36459; MUID:90355967; PMID:2201894

A;Accession: A36459

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-225 <EDM>

A;Cross-references: GB:M34606; NID:g167397; PIDN:AAA33076.1; PID:g167398

C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase homology

C;Keywords: glycosyltransferase; pentosyltransferase

F;2-201/Domain: orotate phosphoribosyltransferase homology <OPT>

Query Match 41.9%; Score 485; DB 2; Length 225;

Best Local Similarity 46.3%; Pred. No. 1.6e-32;

Matches 107; Conservative 45; Mismatches 63; Indels 16; Gaps 7;

Qy 2 SLEKYQTELIEHGMTAGALKFGTFTLKSGRTSPYFFNAGLLASGPVLDLTLC SAYAAT IAR 61
: : : | : | | | | | | | | | | | | : | | :

Db 5 ALDSAKVAFIEAAIEHGVLLFGNFTLKSGRQSPYFFNAGLLYSSSLLSTTAQAYAKVL-- 62

[illegible]

Db 63 ---SSSRIPDFDVLFGPAYKGISLA AVSAVSLYQQTGKD IGYCYNRKEKKDHGEGGTMVG 119

Qy 122 APVRGKRVLVLDVATAGTAIRQAIETV-TKEGGEVVGAVLMLDRQEVGK--EGKSTLAE 178
| | : | | : : : | | : | | : | : : : : : : : | | : | | : |

Db 120 APLKG-RIVIIDDVLTSGKAIREAIDILKASPEAKLVGIVQLVDRQEKQSGSGKSTVQE 178

Qy 179 VEALLGGKGRVPT--ILRMKDLMKWLQEHGRTE-ELAKMQEYWEQYGAKES 226

Db 179 VEEFEG----VPVEPIIGLDDIVKYLESSGKWEKELQEV RKYRAEYGVQRS 225

RESULT 1

PYRE_CRYNE

ID PYRE_CRYNE STANDARD; PRT; 225 AA.
AC P18132;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRT) (OPRTase).
GN URA5.
OS *Cryptococcus neoformans* (*Filobasidiella neoformans*).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; *Filobasidiella*.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90355967; PubMed=2201894;
RA Edman J.C., Kwon-Chung K.J.;
RT "Isolation of the URA5 gene from *Cryptococcus neoformans* var.
RT *neoformans* and its use as a selective marker for transformation."
RL Mol. Cell. Biol. 10:4538-4544(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=J15, J17, J19, J21, J25, and J26;
RA Chen F., Chen L.C., Currie B.P., Spitzer S.G., Spitzer E.D.,
RA Casadevall A.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C5, C7, C24, C25, E4, E9, and E12;
RA Franzot S.P., Hamdan J.S., Casadevall A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=184, 3502, H99, and ATCC 24064;
RA Franzot S.P., Fries B.C., Casadevall A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate = orotate
CC + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: Pyrimidine biosynthesis; fifth step.
CC -!- SIMILARITY: Belongs to the purine/pyrimidine
CC phosphoribosyltransferase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34606; AAA33076.1; -.
DR EMBL; L38582; AAA99182.1; -.
DR EMBL; L38583; AAA99183.1; -.
DR EMBL; L38584; AAA99184.1; -.
DR EMBL; L38585; AAA99185.1; -.
DR EMBL; L38586; AAA99186.1; -.
DR EMBL; L38587; AAA99187.1; -.

DR EMBL; L38588; AAA99188.1; -.
 DR EMBL; U67723; AAB17140.1; -.
 DR EMBL; U67724; AAB17141.1; -.
 DR EMBL; U67725; AAB17142.1; -.
 DR EMBL; U67726; AAB17143.1; -.
 DR EMBL; U67728; AAB17145.1; -.
 DR EMBL; U67730; AAB17147.1; -.
 DR EMBL; U67731; AAB17148.1; -.
 DR EMBL; AF032430; AAB86885.1; -.
 DR EMBL; AF032432; AAB86887.1; -.
 DR EMBL; AF032434; AAB86889.1; -.
 DR EMBL; AF032436; AAB86891.1; -.
 DR PIR; A36459; A36459.
 DR HSSP; P00495; 1ORO.
 DR InterPro; IPR004467; Or_phospho_trans.
 DR InterPro; IPR002375; Pr/py_rp_transf.
 DR InterPro; IPR000836; PRTransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR TIGRFAMs; TIGR00336; pyrE; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW Pyrimidine biosynthesis; Transferase; Glycosyltransferase.
 FT ACT_SITE 109 109 BY SIMILARITY.
 FT VARIANT 8 8 S -> F (IN STRAIN J21).
 FT VARIANT 11 11 V -> I (IN STRAINS J15, J17, J24, J25,
 FT C5, C7, C24, E4, E9, E12, H99, 184 AND
 FT ATCC 24064).
 FT VARIANT 57 57 A -> G (IN STRAINS J26 AND J19).
 FT VARIANT 69 69 D -> N (IN STRAIN J25).
 SQ SEQUENCE 225 AA; 24419 MW; A36EEF8D54CDEB81 CRC64;

Query Match 41.9%; Score 485; DB 1; Length 225;
 Best Local Similarity 46.3%; Pred. No. 1.3e-29;
 Matches 107; Conservative 45; Mismatches 63; Indels 16; Gaps 7;

Qy 2 SLEKYQTELIEHGMTAGALKFGTFTLKSGRTSPYFFNAGLLASGPVLDLCSAYAATIAAR 61
 :|: : || : | | | | | | | | | | | | | | :| | ||| :
 Db 5 ALDSAKVAFIEAAIEHGVLLFGNFTLKSGRQSPYFFNAGLLYSSSLLSTTAQAYAKVL-- 62

 Qy 62 ALKASPGLPAFDVLFPGPAYKGIPFAAGTALLLHRDHGITVGFAYDRKEAKDHGEGGILVG 121
 :| :| | | | | | | | | | | | | | :|: |: :| :|: | | | | | :||
 Db 63 ---SSSRIPDFDVLFGPAYKGISLAAVSAVSLYQQTGKDIGYCYNRKEKKDHGEGGTMVG 119

 Qy 122 APVRGKRVLVLDDVATAGTAIRQAIETV-TKEGGEVVGAVLMLDRQEVGK--EGKSTLAE 178
 ||::| |:::| | :| |||:|: : :|| | :| ||| | : |||: |
 Db 120 APLKG-RIVIIDDLTSGKAIREAIDILKASPEAKLVGIVQLVDRQEKQSGSGKSTVQE 178

 Qy 179 VEALLGGKGRVPT--ILRMKDLMKWLQEHGRTE-ELAKMQEYWEQYGAKE 226
 || | || : : |:|:|: | : | || :::| :|| : |
 Db 179 VEEFEG----VPVEPIIGLDDIVKYLESSGKWEKELQEVRYRAEYGVQRS 225

074686

Query Match 44.6%; Score 516.5; DB 3; Length 244;
Best Local Similarity 47.0%; Pred. No. 6.8e-32;
Matches 110; Conservative 41; Mismatches 72; Indels 11; Gaps 3;

Qy	3	LEKYQTELIEHGMTAGALKFGTFTLKSGRTSPYFFNAGLLASGPVLDTLCSAYAATIARA	62
		: : : : : :	
Db	11	LPAYKTTFLESCLSANVLKFGVFTLKSGRKSPYFFNAGLFHTSSLLSAISTAYANTIVSY	70
Qy	63	LKASPLPAFDVLFPGPAYKGIPFAAGTALLLRDHGKIT---VGFAFYDRKEAKDHGEGGIL	119
		: : : : : : : :	
Db	71	LASNPSILKPDVIFGPGPAYKGIPLACATLLELRHMDPATWSSVSYSYNRKEAKDHGEGGSI	130
Qy	120	VGAPVRGKRVLVLDVATAGTAIRQAIETVTKEGGEVVGAVLMLDRQEVGKEGKSTLAEV	179
		: : : : : : :	
Db	131	VGSPLKGKNVLVIDDVITAGTAMRETLKLVDKEGGKVVGFFVALDRQEKMPGPKDVETDD	190
Qy	180	EALLGGKGR-----VPT--ILRMKDLMKWLQEHGRTEELAKMQEYWEQYGAKE	225
		: : : : : : : : : :	
Db	191	EPRMSAMGOIROEFGVPTASIVTLQDLITLMGTGKNKEDMDRLEEYRCRYRASD	244

Seq ID No. 2

(seam A SID 3 similar)

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID		Description
	1	684	100.0	684	6	AX078058	AX078058 Sequence
	2	613	89.6	3448	6	AX078057	AX078057 Sequence
	3	152.6	22.3	877	8	S47907	S47907 PYR1=orotat
c	4	152.6	22.3	8392	1	AF447860	AF447860 Methyloco
c	5	152.6	22.3	11175	1	AE014701	AE014701 Bifidobac

c	6	152.6	22.3	349980	6	AX492784	AX492784 Sequence
c	7	152.6	22.3	349980	6	AX553951	AX553951 Sequence
	8	149	21.8	1246	8	SFIURA5A	M26957 Sordaria ma
c	9	147.6	21.6	3123	1	PAU38241	U38241 Pseudomonas
c	10	147.6	21.6	10384	1	AE004945	AE004945 Pseudomon
c	11	139.4	20.4	21337	1	AE008873	AE008873 Salmonell
	12	139	20.3	645	1	STOPPRBST	Z19547 S.typhimuri
	13	137.8	20.1	245050	1	AL627280	AL627280 Salmonell
	14	137.8	20.1	300102	1	AE016847	AE016847 Salmonell

Database : N_Geneseq_29Jan04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	684	100.0	684	4	AAF26442			Aaf26442 T. versic
	2	613	89.6	3448	4	AAF26441			Aaf26441 T. versic
c	3	152.6	22.3	349980	6	ABQ81846			Abq81846 Bifidobac
	4	147.6	21.6	642	7	ACA42772			Aca42772 Prokaryot
	5	136.8	20.0	642	7	ACA52250			Aca52250 Prokaryot
	6	136.6	20.0	639	7	ACA49127			Aca49127 Prokaryot
	7	130	19.0	639	7	ACA32096			Aca32096 Prokaryot
	8	125.2	18.3	639	7	ACA35089			Aca35089 Prokaryot
	9	114.4	16.7	642	4	AAF87980			Aaf87980 E. coli o
	10	114.4	16.7	642	7	ACA32692			Aca32692 Prokaryot
c	11	114.4	16.7	3066	5	AAS79981			Aas79981 DNA encod
	12	114.4	16.7	3066	5	AAS89140			Aas89140 DNA encod
c	13	114.4	16.7	3066	5	AAS88527			Aas88527 DNA encod
	14	110.6	16.2	642	3	AAZ53093			Aaz53093 Neisseria
	15	110.2	16.1	642	3	AAZ53094			Aaz53094 Neisseria
	16	110	16.1	47475	3	AAA81465			Aaa81465 N. mening
	17	110	16.1	110000	3	AAA81489_5			Continuation (6 of
	18	110	16.1	349980	3	AAF21612			Aaf21612 Neisseria
	19	109	15.9	744	8	ADA29632			Ada29632 DNA encod
	20	107.4	15.7	1201	5	ABL41545			Abl41545 URA5 gene

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	147.6	21.6	669	4	US-09-252-991A-7270	Sequence 7270, Ap
	2	147.6	21.6	780	4	US-09-252-991A-7431	Sequence 7431, Ap
	3	140.2	20.5	522	4	US-09-252-991A-7206	Sequence 7206, Ap
	4	125.6	18.4	834	4	US-09-489-039A-3429	Sequence 3429, Ap
	5	109	15.9	744	4	US-09-328-352-919	Sequence 919, App
c	6	104.4	15.3	405	4	US-09-252-991A-7491	Sequence 7491, Ap
	7	89	13.0	31063	4	US-09-596-002-20	Sequence 20, Appl
c	8	79.4	11.6	7218	1	US-08-232-463-14	Sequence 14, Appl
	9	70.8	10.4	1926	4	US-09-249-585A-2	Sequence 2, Appli
	10	70.8	10.4	1926	4	US-09-410-399-3	Sequence 3, Appli
	11	70.8	10.4	2580	3	US-09-050-863-2	Sequence 2, Appli

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	149.2	21.8	682	14	CF932870	CF932870 TrEST-B21
	2	134.6	19.7	632	14	CD486120	CD486120 CFUS6.2F0
c	3	113.6	16.6	506	14	CD293012	CD293012 StrPu536.
	4	108.2	15.8	616	14	CB826279	CB826279 rw23d06.y
	5	103.6	15.1	284	12	BM868752	BM868752 mgns001xN
	6	95.4	13.9	484	14	CB279846	CB279846 ru88b12.y
	7	93.4	13.7	654	12	BI955525	BI955525 HVSMEm002
	8	91	13.3	380	13	BQ140776	BQ140776 NF042H05P
	9	86.6	12.7	751	28	BZ570207	BZ570207 msh2_1230
	10	84	12.3	723	14	CB024739	CB024739 TgESTzyc1
c	11	79.2	11.6	1168	12	BM468388	BM468388 AGENCOURT
c	12	78.4	11.5	1292	13	BQ070431	BQ070431 AGENCOURT
c	13	76.2	11.1	975	13	BU171307	BU171307 AGENCOURT
	14	75.6	11.1	970	1		

RESULT 1
 AX078058
 LOCUS AX078058 684 bp DNA linear PAT 22-FEB-2001
 DEFINITION Sequence 2 from Patent WO0107620.
 ACCESSION AX078058
 VERSION AX078058.1 GI:13157813
 KEYWORDS .
 SOURCE Trametes versicolor
 ORGANISM Trametes versicolor
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Aphyllophorales; Trametes.
 REFERENCE 1
 AUTHORS Pfaller, R.
 TITLE PyrF gene and the utilization thereof
 JOURNAL Patent: WO 0107620-A 2 01-FEB-2001;
 Consortium fuer elektrochemische Industrie GmbH (DE)
 FEATURES Location/Qualifiers
 source 1. .684
 /organism="Trametes versicolor"
 /mol_type="unassigned DNA"
 /db_xref="taxon:5325"
 CDS 1. .684
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 /db_xref="REMTREMBL:CAC32408"
 /translation="MSLEKYQTELIEHGMTAGALKFGTFTLKSGRTSPYFFNAGLLAS
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 LMLDRQEVGKEGKSTLAEVEALLGGKGRVPTILRMKDLMKWLQEHGRTEELAKMQEYW
 EQYGAKESE"

ORIGIN

Query Match 100.0%; Score 684; DB 6; Length 684;
 Best Local Similarity 100.0%; Pred. No. 5.2e-80;
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTCGCTCGAAAAATACCAGACAGAGCTCATCGAGCACGGCATGACCGCCGGTGCGCTC	60
Db	1	ATGTCGCTCGAAAAATACCAGACAGAGCTCATCGAGCACGGCATGACCGCCGGTGCGCTC	60
Qy	61	AAGTTCGGGACCTTCACCCTCAAATCAGGCCGGACCTCGCCCTACTTCTTCAACGCCGGC	120
Db	61	AAGTTCGGGACCTTCACCCTCAAATCAGGCCGGACCTCGCCCTACTTCTTCAACGCCGGC	120
Qy	121	CTGCTCGCGTCCGGGCCCCGTGCTCGACACGCTGTGCTCCGCGTACGCCGCGACGATCGCG	180
Db	121	CTGCTCGCGTCCGGGCCCCGTGCTCGACACGCTGTGCTCCGCGTACGCCGCGACGATCGCG	180
Qy	181	CGCGCGCTCAAGGCGTCGCCCCGGGCTGCCCCGCTTCGACGTGCTCTTCGGGCCCCGCTAC	240
Db	181	CGCGCGCTCAAGGCGTCGCCCCGGGCTGCCCCGCTTCGACGTGCTCTTCGGGCCCCGCTAC	240
Qy	241	AAGGGCATCCCGTTTCGCGGCGGGGACCGCGCTGCTGCTGCACCGCGACCACGGGCATCACC	300
Db	241	AAGGGCATCCCGTTTCGCGGCGGGGACCGCGCTGCTGCTGCACCGCGACCACGGGCATCACC	300

Qy	301	GTCGGGTTTCGCGTACGACCGCAAGGAGGCGAAGGATCATGGGGAGGGCGGGATACTTGTG	360
Db	301	GTCGGGTTTCGCGTACGACCGCAAGGAGGCGAAGGATCATGGGGAGGGCGGGATACTTGTG	360
Qy	361	GGCGCGCCGGTGAGGGGCAAGCGCGTGCTGGTGCTGGACGACGTCGCGACGGCGGGCACG	420
Db	361	GGCGCGCCGGTGAGGGGCAAGCGCGTGCTGGTGCTGGACGACGTCGCGACGGCGGGCACG	420
Qy	421	GCGATCCGCCAGGCGATTGAGACTGTGACGAAGGAGGGGGCGAGGTCGTTGGCGCGGTG	480
Db	421	GCGATCCGCCAGGCGATTGAGACTGTGACGAAGGAGGGGGCGAGGTCGTTGGCGCGGTG	480
Qy	481	TTGATGCTCGATCGGCAGGAGGTGGGCAAGGAGGGGAAGAGCACGCTTGCGGAGGTGGAG	540
Db	481	TTGATGCTCGATCGGCAGGAGGTGGGCAAGGAGGGGAAGAGCACGCTTGCGGAGGTGGAG	540
Qy	541	GCGCTGTTGGGCGGGAAGGGACGTGTGCCGACGATCCTGAGGATGAAGGACCTCATGAAG	600
Db	541	GCGCTGTTGGGCGGGAAGGGACGTGTGCCGACGATCCTGAGGATGAAGGACCTCATGAAG	600
Qy	601	TGGTTGCAGGAGCACGGCCGGACGGAGGAGCTTGCGAAGATGCAAGAGTACTGGGAGCAG	660
Db	601	TGGTTGCAGGAGCACGGCCGGACGGAGGAGCTTGCGAAGATGCAAGAGTACTGGGAGCAG	660
Qy	661	TACGGCGCGAAGGAAAAGCGAATGA	684
Db	661	TACGGCGCGAAGGAAAAGCGAATGA	684

RESULT 3

S47907

LOCUS S47907 877 bp DNA linear PLN 08-MAY-1993

DEFINITION PYR1=orotate phosphoribosyl transferase [Colletotrichum graminicola, Genomic, 877 nt].

ACCESSION S47907

VERSION S47907.1 GI:259366

KEYWORDS .

SOURCE Glomerella graminicola

ORGANISM Glomerella graminicola

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Glomerella.

REFERENCE 1 (bases 1 to 877)

AUTHORS Rasmussen,J.B., Panaccione,D.G., Fang,G.C. and Hanau,R.M.

TITLE The PYR1 gene of the plant pathogenic fungus Colletotrichum graminicola: selection by intraspecific complementation and sequence analysis

JOURNAL Mol. Gen. Genet. 235 (1), 74-80 (1992)

MEDLINE 93062810

PUBMED 1435732

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 117372] from the original journal article. This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source

1..877
/organism="Glomerella graminicola"
/mol_type="genomic DNA"
/db_xref="taxon:31870"

gene

114..815
/gene="PYR1"

CDS

/note="orotate phosphoribosyl transferase, OPRTase"
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/gene="PYR1"
/note="This sequence comes from Fig. 2; OPRTase"
/codon_start=1
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/protein_id="AAB24061.1"
/db_xref="GI:259367"
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RADLLRAISLAYAHTVIEAREATGLDFDVVFGPAYKGIPLATSTTDKLAELDPARYGT
TCYSFDRKEAKDHGEGGNIVGAPLKGQKVLIVDDVITAGTAKREAIKIRKEGGEVVG
IVVALDRMEKLPADGDDSKPGPSALGEIKKEYGIPIFSILTDDIIEGAKSFASAED
IKRTEEYRAKYKATD"

ORIGIN

Query Match 22.3%; Score 152.6; DB 8; Length 877;

Best Local Similarity 61.5%; Pred. No. 6.9e-11;

Matches 286; Conservative 0; Mismatches 164; Indels 15; Gaps 2;

Qy 46 ACCGCCGGTGCCTCAAGTTCGGGACCTTCACCCCTCAAATCAGGCCGGACCTCGCCCTAC 105

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 162 ATCGCCGGCGTCCTGAAGTTCGGCTCCTTCGAGCTCAAGTCGAAGCGCATCTCCCCCTAC 221

Qy 106 TTCTTCAACGCCGGCCTGCTCGCGTCCGGGCCCCGTGCTCGACACGCTGTGCTCCGCGTAC 165

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 222 TTCTTCAACGCCGGCGACTTCTACCGCGCTGACCTCCTGCGCGCCATCTCTCTCGCCTAT 281

Qy	166	GCCGCGACGATCAGCGCGCGCTCAAGGCCTCGCCC GGCTGCCCGCGTTTCGACGTGCTC	225
Db	282	GCCACACCGTCATCGAGGCGCGGAGGCCACCGGC-----CTCGACTTCGACGTCGTC	335
Qy	226	TTCGGGCCCCGCGTACAAGGGCATCCCGTTCGCGGCGGGGACC GC-----GCTGCTG	276
Db	336	TTCGGCCCCGGCCTACAAGGGCATCCCCCTCGCGACCTCTACCACTGACAAGCTCGCCGAG	395
Qy	277	CTGCACCGCGACCACGGCATCACCGTTCGGGTTCGCGTACGACCGCAAGGAGGCGAAGGAT	336
Db	396	CTCGACCCGGCCCCGCTACGGCACCACTGCTACTCTTCGACCGCAAGGAGGCCAAGGAC	455
Qy	337	CATGGGGAGGGCGGGGATACTTG TGGGCGCGCCGGTGAGGGGCAAGCGCGTGCTGGTGCTG	396
Db	456	CACGGCGAGGGCGGGCAACATTGTCTGGAGCGCCCCCTCAAGGGCCAGAAGGTTCTGATCGTT	515
Qy	397	GACGACGTCGCGACGGCGGGCACGGCGATCCGCCAGGCGATTGAGACTGTGACGAAGGAG	456
Db	516	GACGACGTCATCACC GCCGGCACCGCCAAGCGGAGGCCATCGCCAAGATCCGTAAGGAA	575
Qy	457	GGGGGCGAGGTTCGTTGGCGCGGTGTTGATGCTCGATCGGCAGGAG	501
Db	576	GGCGGCGAGGTTCGTCGGCATCGTCGTCGCGCTGGACCGTATGGAG	620

Sequence Alignment Results B

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 14, 2004, 03:17:27 ; Search time 40 Seconds
(without alignments)
545.887 Million cell updates/sec

Title: US-10-031-547-3
Perfect score: 1158
Sequence: 1 MSLEKYQTELIEHGMTAGAL.....TEELAKMQEYWEQYGAKESE 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	485	41.9	225	2 A36459	orotate phosphorib
2	462.5	39.9	226	1 XJBY5	orotate phosphorib
3	458	39.6	213	2 A82981	orotate phosphorib
4	454	39.2	213	2 S32801	orotate phosphorib
5	453	39.1	213	1 XJEC	orotate phosphorib
6	452	39.0	213	2 E91193	orotate phosphorib
7	452	39.0	213	2 F86040	orotate phosphorib
8	452	39.0	214	2 E82350	orotate phosphorib
9	451	38.9	215	2 AF0006	orotate phosphorib
10	449	38.8	233	1 S30118	orotate phosphorib
11	446	38.5	213	2 AH0970	orotate phosphorib
12	446	38.5	215	2 T40667	orotate phosphorib
13	432	37.3	213	2 I64058	orotate phosphorib
14	428.5	37.0	227	1 XJBY10	orotate phosphorib

15	428.5	37.0	232	1	JS0175	orotate phosphorib
16	426	36.8	219	2	S55840	orotate phosphorib
17	422.5	36.5	213	2	H81032	probable orotate p
18	416.5	36.0	231	1	A29459	orotate phosphorib
19	414.5	35.8	236	1	S13091	orotate phosphorib
20	398	34.4	219	2	H82840	orotate phosphorib
21	381.5	32.9	213	2	A84995	orotate phosphorib
22	366	31.6	224	2	C96903	orotate phosphorib
23	218	18.8	458	2	T30520	probable orotate p
24	209	18.0	461	2	T02058	UMP synthase - com
25	207.5	17.9	476	2	S46440	bifunctional UMP s
26	204.5	17.7	476	2	T47606	UMP synthase - Ara
27	203.5	17.6	186	2	B71054	probable orotate p
28	203	17.5	182	2	B75089	probable orotate p
29	197	17.0	182	2	T47129	orotate phosphorib
30	194.5	16.8	195	2	G90208	orotate phosphorib
31	194	16.8	480	1	A30148	UMP synthase - hum
32	188	16.2	480	1	JN0558	UMP synthase - bov
33	181.5	15.7	478	1	S03826	UMP synthase - sli
34	181	15.6	175	2	F84361	orotate phosphorib
35	181	15.6	178	2	D69467	probable orotate p
36	174.5	15.1	178	2	B72463	probable orotate p
37	171.5	14.8	180	2	H69115	probable orotate p
38	170	14.7	209	2	AG1675	orotate phosphorib
39	169.5	14.6	210	2	F97948	orotate phosphorib
40	169.5	14.6	227	2	T33094	probable orotate p
41	166.5	14.4	212	1	A60993	orotate phosphorib
42	165.5	14.3	209	2	D86758	orotate phosphorib
43	165.5	14.3	210	2	D95081	orotate phosphorib
44	160	13.8	209	2	AG1303	orotate phosphorib
45	159	13.7	493	1	JU0141	UMP synthase - fru

Sequence Alignment

Results A

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 2004, 03:08:51 ; Search time 23 Seconds
(without alignments)
513.910 Million cell updates/sec

Title: US-10-031-547-3
Perfect score: 1158
Sequence: 1 MSLEKYQTELIEHGMTAGAL.....TEELAKMQEYWEQYGAKES 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	485	41.9	225	1 PYRE_CRYNE	P18132 cryptococcus
2	464	40.1	215	1 PYRE_SHEON	Q8e915 shewanella
3	462.5	39.9	226	1 PYRE_YEAST	P13298 saccharomyc
4	462	39.9	213	1 PYRE_VIBPA	Q87t92 vibrio para
5	460.5	39.8	226	1 PYRE_KLULA	O13474 kluyveromyc
6	458	39.6	213	1 PYRE_PSEAE	P50587 pseudomonas
7	458	39.6	213	1 PYRE_VIBVU	Q8ddx5 vibrio vuln
8	452	39.0	212	1 PYRE_SALTY	P08870 salmonella
9	452	39.0	214	1 PYRE_VIBCH	Q9kvd5 vibrio chol
10	451	38.9	212	1 PYRE_ECOLI	P00495 escherichia
11	451	38.9	215	1 PYRE_YERPE	Q8zjp7 yersinia pe
12	450	38.9	212	1 PYRE_ECO57	Q8xd99 escherichia
13	449	38.8	233	1 PYRE_COLGR	P35788 colletotric
14	449	38.8	238	1 PYRE_COCPO	O93849 coccidioid
15	446	38.5	215	1 PYRE_SCHPO	O94331 schizosacch
16	445	38.4	213	1 PYRE_PSEPK	Q88c92 pseudomonas
17	444	38.3	212	1 PYRE_SALTI	Q8z2h5 salmonella
18	442.5	38.2	183	1 PYRE_METCA	Q8vr31 methylococc

19	435.5	37.6	234	1	PYRE_METAN	Q42767	metarhizium
20	432	37.3	213	1	PYRE_HAEIN	P43855	haemophilus
21	429	37.0	213	1	PYRE_PSESM	Q88bd7	pseudomonas
22	428.5	37.0	227	1	PYRX_YEAST	P30402	saccharomyc
23	428.5	37.0	232	1	PYRE_SORMA	P18904	sordaria ma
24	426	36.8	219	1	PYRE_YARLI	P41923	yarrowia li
25	422.5	36.5	213	1	PYRE_NEIMA	Q9jr25	neisseria m
26	414.5	35.8	236	1	PYRE_TRIRE	P21846	trichoderma
27	413	35.7	214	1	PYRE_PASMU	Q9cjlw4	pasteurella
28	403.5	34.8	231	1	PYRE_PODAN	P08309	podospira a
29	399.5	34.5	219	1	PYRE_XANCP	Q8p469	xanthomonas
30	398	34.4	219	1	PYRE_XYLFA	Q9pgz3	xylella fas
31	398	34.4	231	1	PYRE_BIFLO	Q8g661	bifidobacte
32	397	34.3	219	1	PYRE_XANAC	Q8pfs5	xanthomonas
33	392	33.9	226	1	PYRE_RALSO	Q8y342	ralstonia s
34	391	33.8	219	1	PYRE_XYLFT	Q87f16	xylella fas
35	381.5	32.9	213	1	PYRE_BUCAI	P57622	buchnera ap
36	366	31.6	224	1	PYRE_CLOAB	Q97n11	clostridium
37	272	23.5	206	1	PYRE_BUCBP	P59575	buchnera ap
38	262.5	22.7	193	1	PYRE_PYRAE	Q8ztg3	pyrobaculum
39	239.5	20.7	183	1	PYRE_METKA	P58860	methanopyru
40	218	18.8	197	1	PYRE_SULAC	O08359	sulfolobus
41	212.5	18.4	195	1	PYRE_SULTO	Q970x1	sulfolobus
42	209	18.0	461	1	PYR5_TOBAC	Q42942	nicotiana t
43	204.5	17.7	476	1	PYR5_ARATH	Q42586	arabidopsis
44	203.5	17.6	186	1	PYRE_PYRHO	O58855	pyrococcus
45	203	17.5	182	1	PYRE_PYRAB	P56814	pyrococcus